IN THE CLAIMS:

1. (presently amended) A method of identifying subjects at risk of developing Crohn's disease comprising:

a) providing

i) nucleic acid from a subject, wherein said nucleic acid comprises a Nod2 gene; and

b) detecting the presence or absence of ~~one or more a variations in said~~ a variant Nod2 gene, wherein said variant Nod2 gene has a nucleic acid sequence having a cytosine insertion at position 3124 of SEQ ID NO:1, thereby identifying subjects at risk of developing Crohn's disease.

2. (canceled)

3. (presently amended) The method of Claim ~~2~~1, wherein said ~~determining of step c)~~ identifying subjects at risk of developing Crohn's disease comprises determining a genotype relative risk for said subject.

4. (presently amended) The method of Claim ~~2~~1, wherein said ~~determining of step c)~~ identifying subjects at risk of developing Crohn's disease comprises determining a population attributable risk for said subject.

5-6. (canceled)

7. (presently amended) The method of claim 1, wherein ~~said variation~~ the presence of said variant Nod2 gene results in increased NF-κB activation.

8-10. (canceled)

11. (original) The method of Claim 1, wherein said detecting in step (b) is accomplished by hybridization analysis.

12. (original) The method of Claim 1, wherein said detecting in step (b) comprises comparing the sequence of said nucleic acid to the sequence of a wild-type Nod2 nucleic acid.

13-23. (canceled)

24. (presently amended) A computer implemented method of determining a patient's risk of developing Crohn's disease comprising:

a) providing:

i) nucleic acid from a patient, wherein said nucleic acid comprises a Nod2 gene; and

ii) a computer comprising software for the prediction of a patient's risk of developing Crohn's disease; and

b) detecting the presence of ~~one or more variations in~~ a variant Nod2 gene in said patient~~'s Nod2 gene,~~ wherein said variant Nod2 gene has a nucleic acid sequence having a cytosine insertion at position 3124 of SEQ ID NO:1, to generate genetic variation information;

c) entering said genetic variation information into said computer; and

d) calculating said patient's risk with said software.

25. (original) The method of claim 24, further comprising step e) displaying said patient's risk.

26. (original) The method of Claim 24, wherein said risk comprises a genotype relative risk.

27. (original) The method of Claim 24, wherein said risk comprises a population attributable risk.

28-33. (cancelled)

33. (original) The method of Claim 24, wherein said detecting in step (b) comprises comparing the sequence of said nucleic acid to the sequence of a wild-type Nod2 nucleic acid.

34-37. (canceled)

38. (newly added) The method of claim 1, wherein said variant Nod2 gene has the nucleic acid sequence of SEQ ID NO: 33.

39. (newly added) The method of claim 24, wherein said variant Nod2 gene has the nucleic acid sequence of SEQ ID NO: 33.